

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/211,755ADATE: 03/21/2000
TIME: 16:49:11

INPUT SET: S35062.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Kenneth A. Jones
Thomas M. Laz
Beth Borowsky

(ii) TITLE OF INVENTION: DNA Encoding a GABABR2 Polypeptide And
Uses Thereof

(iii) NUMBER OF SEQUENCES: 55

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Cooper & Dunham LLP
(B) STREET: 1185 Avenue of the Americas
(C) CITY: New York
(D) STATE: New York
(E) COUNTRY: U.S.A.
(F) ZIP: 10036

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 09/211,755
(B) FILING DATE: 15-Dec-1998
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: White Esq., John P.
(B) REGISTRATION NUMBER: 28,678
(C) REFERENCE/DOCKET NUMBER: 54002-D/JPW

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 212-278-0400
(B) TELEFAX: 212-391-0525

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 3244 base pairs

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TC 1600 MAIL ROOM

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47 (B) TYPE: nucleic acid
48 (C) STRANDEDNESS: single
49 (D) TOPOLOGY: linear
50
51 (ii) MOLECULE TYPE: DNA (genomic)
52
53 (iii) HYPOTHETICAL: NO
54
55 (iv) ANTI-SENSE: NO
56
57 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
58
59 TGACCTCGGG GCAGGTCTCTG GTGCAGAGCG TCGCCAAGGA CGCCGAGAGG GAGGCGGGAT 60
60
61 TGCCAGACA TCCTTCAGCG AAGTGCATGT GTGTTTGTA ACCATCGTTG GCTGTGCGGA 120
62
63 GACCGCGAGG ACCGGTCCAG GCTGCGGCGG AGTCGAGGGC GAGGGAGAGG CCGCGTGAGT 180
64
65 GAGCAGAGTC CAGAGCCGTG CGCCCCCAGA ACTGCGCGTC CGCCCCGTGC ACCCCGCGC 240
66
67 GCCATGCCCA GTTGCCCCGC GCGCTCTGCT ACGGGCCCCG TCTCCATCAT GGGCCTCATG 300
68
69 CCGCTACCA AGGAGGTGGC CAAGGGCAGC ATCGGGCGCG GTGTGCTCCC CGCCGTGGAA 360
70
71 CTGGCCATCG AGCAGATCCG CAACGAGTCA CTCCTGCGCC CCTACTTCCT CGACCTGCGG 420
72
73 CTCTATGACA CGGAGTGCGA CAACGCAAAA GGTTTGAAAG CCTTCTACGA TGCGATAAAA 480
74
75 TACGGGCCGA ACCACTTGAT GGTGTTTGGA GGCGTCTGTC CATCCGTCAC ATCCATCATT 540
76
77 GCAGAGTCCC TCCAAGGCTG GAATCTGGTG CAGCTTCTT TTGCTGCAAC CACGCCTGTT 600
78
79 CTAGCCGATA AGAAAAAATA CCCTTATTTT TTTCGGACCG TCCCATCAGA CAATGCGGTG 660
80
81 AATCCAGCCA TTCTGAAGTT GCTCAAGCAC TACAGTGGA AGCGCGTGGG CACGCTGACG 720
82
83 CAAGACGTTT AGAGGTTCTC TGAGGTGCGG AATGACCTGA CTGGAGTTCT GTATGGCGAG 780
84
85 GACATTGAGA TTTCAGACAC CGAGAGCTTC TCCAACGATC CCTGTACCAG TGTCAAAAAG 840
86
87 CTGAAGGGGA ATGATGTGCG GATCATCCTT GGCCAGTTTG ACCAGAATAT GGCAGCAAAA 900
88
89 GTGTTCTGTT GTGCATACGA GGAGAACATG TATGGTAGTA AATATCAGTG GATCATTCCG 960
90
91 GGCTGGTACG AGCCTTCTTG GTGGGAGCAG GTGCACACGG AAGCCAACTC ATCCCCTGTC 1020
92
93 CTCCGGAAGA ATCTGCTTGC TGCCATGGAG GGCTACATTG GCGTGGATTT CGAGCCCCTG 1080
94
95 AGCTCCAAGC AGATCAAGAC CATCTCAGGA AAGACTCCAC AGCAGTATGA GAGAGAGTAC 1140
96
97 AACACAAGC GGTCAAGCGT GGGGCCAGC AAGTTCCACG GGTACGCCTA CGATGGCATC 1200
98
99 TGGGTCATCG CCAAGACACT GCAGAGGGCC ATGGAGACAC TGCATGCCAG CAGCCGGCAC 1260

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100							
101	CAGCGGATCC	AGGACTTCAA	CTACACGGAC	CACACGCTGG	GCAGGATCAT	CCTCAATGCC	1320
102							
103	ATGAACGAGA	CCAACTTCTT	CGGGGTCACG	GGTCAAGTTG	TATTCCGGAA	TGGGGAGAGA	1380
104							
105	ATGGGGACCA	TTAAATTTAC	TCAATTTCAA	GACAGCAGGG	AGGTGAAGGT	GGGAGAGTAC	1440
106							
107	AACGCTGTGG	CCGACACACT	GGAGATCATC	AATGACACCA	TCAGGTTCCA	AGGATCCGAA	1500
108							
109	CCACCAAAAG	ACAAGACCAT	CATCCTGGAG	CAGCTGCGGA	AGATCTCCCT	ACCTCTCTAC	1560
110							
111	AGCATCCTCT	CTGCCCTCAC	CATCCTCGGG	ATGATCATGG	CCAGTGCTTT	TCTCTTCTTC	1620
112							
113	AACATCAAGA	ACCGGAATCA	GAAGCTCATA	AAGATGTCGA	GTCCATACAT	GAACAACCTT	1680
114							
115	ATCATCCTTG	GAGGGATGCT	TTCCTATGCT	TCCATATTTC	TCTTTGGCCT	TGATGGATCC	1740
116							
117	TTTGTCTCTG	AAAAGACCTT	TGAAACACTT	TGCACCGTCA	GGACCTGGAT	TCTCACCGTG	1800
118							
119	GGCTACACGA	CCGCTTTTGG	GGCCATGTTT	GCAAAGACCT	GGAGAGTCCA	CGCCATCTTC	1860
120							
121	AAAAATGTGA	AAATGAAGAA	GAAGATCATC	AAGGACCAGA	AACTGCTTGT	GATCGTGGGG	1920
122							
123	GGCATGCTGC	TGATCGACCT	GTGTATCCTG	ATCTGCTGGC	AGGCTGTGGA	CCCCCTGCGA	1980
124							
125	AGGACAGTGG	AGAAGTACAG	CATGGAGCCG	GACCCAGCAG	GACGGGATAT	CTCCATCCGC	2040
126							
127	CCTCTCCTGG	AGCACTGTGA	GAACACCCAT	ATGACCATCT	GGCTTGGCAT	CGTCTATGCC	2100
128							
129	TACAAGGGAC	TTCTCATGTT	GTTCCGTTGT	TTCTTAGCTT	GGGAGACCCG	CAACGTCAGC	2160
130							
131	ATCCCCGCAC	TCAACGACAG	CAAGTACATC	GGGATGAGTG	TCTACAACGT	GGGGATCATG	2220
132							
133	TGCATCATCG	GGGCCGCTGT	CTCCTTCCTG	ACCCGGGACC	AGCCCAATGT	GCAGTTCTGC	2280
134							
135	ATCGTGCTC	TGGTCATCAT	CTTCTGCAGC	ACCATCACCC	TCTGCCTGGT	ATTCTGTCCG	2340
136							
137	AAGCTCATCA	CCCTGAGAAC	AAACCCAGAT	GCAGCAACGC	AGAACAGGCG	ATTCCAGTTC	2400
138							
139	ACTCAGAATC	AGAAGAAAGA	AGATTCTAAA	ACGTCCACCT	CGGTCACCAG	TGTGAACCAA	2460
140							
141	GCCAGCACAT	CCCGCCTGGA	GGGCCTACAG	TCAGAAAACC	ATCGCCTGCG	AATGAAGATC	2520
142							
143	ACAGAGCTGG	ATAAAGACTT	GGAAGAGGTC	ACCATGCAGC	TGCAGGACAC	ACCAGAAAAG	2580
144							
145	ACCACCTACA	TTAAACAGAA	CCACTACCAA	GAGCTCAATG	ACATCCTCAA	CCTGGGAAAC	2640
146							
147	TTCACTGAGA	GCACAGATGG	AGGAAAGGCC	ATTTTAAAAA	ATCACCTCGA	TCAAAATCCC	2700
148							
149	CAGCTACAGT	GGAACACAAC	AGAGCCCTCT	CGAACATGCA	AAGATCCTAT	AGAAGATATA	2760
150							
151	AACTCTCCAG	AACACATCCA	GCGTCGGCTG	TCCCTCCAGC	TCCCCATCCT	CCACCACGCC	2820
152							

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153 TACCTCCCAT CCATCGGAGG CGTGGACGCC AGCTGTGTCA GCCCCTGCGT CAGCCCCACC 2880
154
155 GCCAGCCCCC GCCACAGACA TGTGCCACCC TCCTTCCGAG TCATGGTCTC GGGCCTGTAA 2940
156
157 GGGTGGGAGG CCTGGGCCCCG GGGCCTCCCC CGTGACAGAA CCACACTGGG CAGAGGGGTC 3000
158
159 TGCTGCAGAA AACTGTTCGG CTCTGGCTGC GGAGAAGCTG GGCACCATGG CTGGCCTCTC 3060
160
161 AGGACCACTC GGATGGCACT CAGGTGGACA GGACGGGGCA GGGGGAGACT TGGCACCTGA 3120
162
163 CCTCGAGCCT TATTTGTGAA GTCCTTATTT CTTACAAAAG AAGAGGAACG GAAATGGGAC 3180
164
165 GTCTTCCTTA ACATCTGCAA ACAAGGAGGC GCTGGGATAT CAAACTTGCA AAAAAAAAAA 3240
166
167 AAAA 3244
168
169

```

(2) INFORMATION FOR SEQ ID NO:2:

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172 (i) SEQUENCE CHARACTERISTICS:
173 (A) LENGTH: 898 amino acids
174 (B) TYPE: amino acid
175 (C) STRANDEDNESS: single
176 (D) TOPOLOGY: linear
177

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178 (ii) MOLECULE TYPE: DNA (genomic)
179

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180 (iii) HYPOTHETICAL: NO
181

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182 (iv) ANTI-SENSE: NO
183

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184 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
185

```

```

186 Met Pro Ser Cys Pro Ala Arg Ser Ala Thr Gly Pro Leu Ser Ile Met
187 1 5 10 15
188
189 Gly Leu Met Pro Leu Thr Lys Glu Val Ala Lys Gly Ser Ile Gly Arg
190 20 25 30
191
192 Gly Val Leu Pro Ala Val Glu Leu Ala Ile Glu Gln Ile Arg Asn Glu
193 35 40 45
194
195 Ser Leu Leu Arg Pro Tyr Phe Leu Asp Leu Arg Leu Tyr Asp Thr Glu
196 50 55 60
197
198 Cys Asp Asn Ala Lys Gly Leu Lys Ala Phe Tyr Asp Ala Ile Lys Tyr
199 65 70 75 80
200
201 Gly Pro Asn His Leu Met Val Phe Gly Gly Val Cys Pro Ser Val Thr
202 85 90 95
203
204 Ser Ile Ile Ala Glu Ser Leu Gln Gly Trp Asn Leu Val Gln Leu Ser
205 100 105 110

```

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206																			
207	Phe	Ala	Ala	Thr	Thr	Pro	Val	Leu	Ala	Asp	Lys	Lys	Lys	Tyr	Pro	Tyr			
208			115					120					125						
209																			
210	Phe	Phe	Arg	Thr	Val	Pro	Ser	Asp	Asn	Ala	Val	Asn	Pro	Ala	Ile	Leu			
211		130					135					140							
212																			
213	Lys	Leu	Leu	Lys	His	Tyr	Gln	Trp	Lys	Arg	Val	Gly	Thr	Leu	Thr	Gln			
214	145					150					155					160			
215																			
216	Asp	Val	Gln	Arg	Phe	Ser	Glu	Val	Arg	Asn	Asp	Leu	Thr	Gly	Val	Leu			
217					165					170					175				
218																			
219	Tyr	Gly	Glu	Asp	Ile	Glu	Ile	Ser	Asp	Thr	Glu	Ser	Phe	Ser	Asn	Asp			
220				180					185					190					
221																			
222	Pro	Cys	Thr	Ser	Val	Lys	Lys	Leu	Lys	Gly	Asn	Asp	Val	Arg	Ile	Ile			
223			195					200					205						
224																			
225	Leu	Gly	Gln	Phe	Asp	Gln	Asn	Met	Ala	Ala	Lys	Val	Phe	Cys	Cys	Ala			
226		210					215					220							
227																			
228	Tyr	Glu	Glu	Asn	Met	Tyr	Gly	Ser	Lys	Tyr	Gln	Trp	Ile	Ile	Pro	Gly			
229	225					230					235					240			
230																			
231	Trp	Tyr	Glu	Pro	Ser	Trp	Trp	Glu	Gln	Val	His	Thr	Glu	Ala	Asn	Ser			
232					245					250					255				
233																			
234	Ser	Arg	Cys	Leu	Arg	Lys	Asn	Leu	Leu	Ala	Ala	Met	Glu	Gly	Tyr	Ile			
235				260				265						270					
236																			
237	Gly	Val	Asp	Phe	Glu	Pro	Leu	Ser	Ser	Lys	Gln	Ile	Lys	Thr	Ile	Ser			
238			275					280					285						
239																			
240	Gly	Lys	Thr	Pro	Gln	Gln	Tyr	Glu	Arg	Glu	Tyr	Asn	Asn	Lys	Arg	Ser			
241		290					295					300							
242																			
243	Gly	Val	Gly	Pro	Ser	Lys	Phe	His	Gly	Tyr	Ala	Tyr	Asp	Gly	Ile	Trp			
244	305					310					315				320				
245																			
246	Val	Ile	Ala	Lys	Thr	Leu	Gln	Arg	Ala	Met	Glu	Thr	Leu	His	Ala	Ser			
247					325					330					335				
248																			
249	Ser	Arg	His	Gln	Arg	Ile	Gln	Asp	Phe	Asn	Tyr	Thr	Asp	His	Thr	Leu			
250				340					345					350					
251																			
252	Gly	Arg	Ile	Ile	Leu	Asn	Ala	Met	Asn	Glu	Thr	Asn	Phe	Phe	Gly	Val			
253			355				360						365						
254																			
255	Thr	Gly	Gln	Val	Val	Phe	Arg	Asn	Gly	Glu	Arg	Met	Gly	Thr	Ile	Lys			
256		370					375					380							
257																			
258	Phe	Thr	Gln	Phe	Gln	Asp	Ser	Arg	Glu	Val	Lys	Val	Gly	Glu	Tyr	Asn			

INPUT SET: S35062.raw

***** PREVIOUSLY ERRORED SEQUENCES - EDITED *****

897 (2) INFORMATION FOR SEQ ID NO:17:

898

899 (i) SEQUENCE CHARACTERISTICS:

900 (A) LENGTH: 26 base pairs

901 (B) TYPE: nucleic acid

902 (C) STRANDEDNESS: single

903 (D) TOPOLOGY: linear

904

905 (ii) MOLECULE TYPE: other nucleic acid

906

907 (iii) HYPOTHETICAL: NO

908

909 (iv) ANTI-SENSE: NO

910

911 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

912

913 TCATGCCGCT CACCAAGGAG GTGGCC

26

914

915

935 (2) INFORMATION FOR SEQ ID NO:19:

936

937 (i) SEQUENCE CHARACTERISTICS:

938 (A) LENGTH: 24 base pairs

939 (B) TYPE: nucleic acid

940 (C) STRANDEDNESS: single

941 (D) TOPOLOGY: linear

942

943 (ii) MOLECULE TYPE: other nucleic acid

944

945 (iii) HYPOTHETICAL: NO

946

947 (iv) ANTI-SENSE: NO

948

949 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

950

951 TGAGTGAGCA GAGTCCAGAG CCGT

24

952

953

1954 (2) INFORMATION FOR SEQ ID NO:55:

1955

1956 (i) SEQUENCE CHARACTERISTICS:

1957 (A) LENGTH: 844 amino acids

1958 (B) TYPE: amino acid

1959 (C) STRANDEDNESS:

1960 (D) TOPOLOGY: Not Relevant

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1961
1962 (ii) MOLECULE TYPE: peptide
1963
1964 (iii) HYPOTHETICAL: NO
1965
1966
1967 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
1968
1969 Met Gly Pro Gly Gly Pro Cys Thr Pro Val Gly Trp Pro Leu Pro Leu
1970 1 5 10 15
1971
1972 Leu Leu Val Met Ala Ala Gly Val Ala Pro Val Trp Ala Ser His Ser
1973 20 25 30
1974
1975 Pro His Leu Pro Arg Pro His Pro Arg Val Pro Pro His Pro Ser Ser
1976 35 40 45
1977
1978 Glu Arg Arg Ala Val Tyr Ile Gly Ala Leu Phe Pro Met Ser Gly Gly
1979 50 55 60
1980
1981 Trp Pro Gly Gly Gln Ala Cys Gln Pro Ala Val Glu Met Ala Leu Glu
1982 65 70 75 80
1983
1984 Asp Val Asn Ser Arg Arg Asp Ile Leu Pro Asp Tyr Glu Leu Lys Leu
1985 85 90 95
1986
1987 Ile His His Asp Ser Lys Cys Asp Pro Gly Gln Ala Thr Lys Tyr Leu
1988 100 105 110
1989
1990 Tyr Glu Leu Leu Tyr Asn Asp Pro Ile Lys Ile Ile Leu Met Pro Gly
1991 115 120 125
1992
1993 Cys Ser Ser Val Ser Thr Leu Val Ala Glu Ala Ala Arg Met Trp Asn
1994 130 135 140
1995
1996 Leu Ile Val Leu Ser Tyr Gly Ser Ser Ser Pro Ala Leu Ser Asn Arg
1997 145 150 155 160
1998
1999 Gln Arg Phe Pro Thr Phe Phe Arg Thr His Pro Ser Ala Thr Leu His
2000 165 170 175
2001
2002 Asn Pro Thr Arg Val Lys Leu Phe Glu Lys Trp Gly Trp Lys Lys Ile
2003 180 185 190
2004
2005 Ala Thr Ile Gln Gln Thr Thr Glu Val Phe Thr Ser Thr Leu Asp Asp
2006 195 200 205
2007
2008 Leu Glu Glu Arg Val Lys Glu Ala Gly Ile Glu Ile Thr Phe Arg Gln
2009 210 215 220
2010
2011 Ser Phe Phe Ser Asp Pro Ala Val Pro Val Lys Asn Leu Lys Arg Gln
2012 225 230 235 240
2013

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2014	Asp	Ala	Arg	Ile	Ile	Val	Gly	Leu	Phe	Tyr	Glu	Thr	Glu	Ala	Arg	Lys
2015					245					250						255
2016																
2017	Val	Phe	Cys	Glu	Val	Tyr	Lys	Glu	Arg	Leu	Phe	Gly	Lys	Lys	Tyr	Val
2018				260					265						270	
2019																
2020	Trp	Phe	Leu	Ile	Gly	Trp	Tyr	Ala	Asp	Asn	Trp	Phe	Lys	Thr	Tyr	Asp
2021			275					280					285			
2022																
2023	Pro	Ser	Ile	Asn	Cys	Thr	Val	Glu	Glu	Met	Thr	Glu	Ala	Val	Glu	Gly
2024		290					295					300				
2025																
2026	His	Ile	Thr	Thr	Glu	Ile	Val	Met	Leu	Asn	Pro	Ala	Asn	Thr	Arg	Ser
2027	305					310					315					320
2028																
2029	Ile	Ser	Asn	Met	Thr	Ser	Gln	Glu	Phe	Val	Glu	Lys	Leu	Thr	Lys	Arg
2030					325					330					335	
2031																
2032	Leu	Lys	Arg	His	Pro	Glu	Glu	Thr	Gly	Gly	Phe	Gln	Glu	Ala	Pro	Leu
2033				340					345					350		
2034																
2035	Ala	Tyr	Asp	Ala	Ile	Trp	Ala	Leu	Ala	Leu	Ala	Leu	Asn	Lys	Thr	Ser
2036			355					360					365			
2037																
2038	Gly	Gly	Gly	Gly	Arg	Ser	Gly	Val	Arg	Leu	Glu	Asp	Phe	Asn	Tyr	Asn
2039		370					375					380				
2040																
2041	Asn	Gln	Thr	Ile	Thr	Asp	Gln	Ile	Tyr	Arg	Ala	Met	Asn	Ser	Ser	Ser
2042	385					390					395					400
2043																
2044	Phe	Glu	Gly	Val	Ser	Gly	His	Val	Val	Phe	Asp	Ala	Ser	Gly	Ser	Arg
2045					405					410					415	
2046																
2047	Met	Ala	Trp	Thr	Leu	Ile	Glu	Gln	Leu	Gln	Gly	Gly	Ser	Tyr	Lys	Lys
2048				420					425					430		
2049																
2050	Ile	Gly	Tyr	Tyr	Asp	Ser	Thr	Lys	Asp	Asp	Leu	Ser	Trp	Ser	Lys	Thr
2051			435					440					445			
2052																
2053	Asp	Lys	Trp	Ile	Gly	Gly	Ser	Pro	Pro	Ala	Asp	Gln	Thr	Leu	Val	Ile
2054		450					455					460				
2055																
2056	Lys	Thr	Phe	Arg	Phe	Leu	Ser	Gln	Lys	Leu	Phe	Ile	Ser	Val	Ser	Val
2057	465					470					475					480
2058																
2059	Leu	Ser	Ser	Leu	Gly	Ile	Val	Leu	Ala	Val	Val	Cys	Leu	Ser	Phe	Asn
2060					485					490					495	
2061																
2062	Ile	Tyr	Asn	Ser	His	Val	Arg	Tyr	Ile	Gln	Asn	Ser	Gln	Pro	Asn	Leu
2063				500					505					510		
2064																
2065	Asn	Asn	Leu	Thr	Ala	Val	Gly	Cys	Ser	Leu	Ala	Leu	Ala	Ala	Val	Phe
2066			515					520					525			

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2067	
2068	Pro Leu Gly Leu Asp Gly Tyr His Ile Gly Arg Ser Gln Phe Pro Phe
2069	530 535 540
2070	
2071	Val Cys Gln Ala Arg Leu Trp Leu Leu Gly Leu Gly Phe Ser Leu Gly
2072	545 550 555 560
2073	
2074	Tyr Gly Ser Met Phe Thr Lys Ile Trp Trp Val His Thr Val Phe Thr
2075	565 570 575
2076	
2077	Lys Lys Glu Glu Lys Lys Glu Trp Arg Lys Thr Leu Glu Pro Trp Lys
2078	580 585 590
2079	
2080	Leu Tyr Ala Thr Val Gly Leu Leu Val Gly Met Asp Val Leu Thr Leu
2081	595 600 605
2082	
2083	Ala Ile Trp Gln Ile Val Asp Pro Leu His Arg Thr Ile Glu Thr Phe
2084	610 615 620
2085	
2086	Ala Lys Glu Glu Pro Lys Glu Asp Ile Asp Val Ser Ile Leu Pro Gln
2087	625 630 635 640
2088	
2089	Leu Glu His Cys Ser Ser Lys Lys Met Asn Thr Trp Leu Gly Ile Phe
2090	645 650 655
2091	
2092	Tyr Gly Tyr Lys Gly Leu Leu Leu Leu Leu Gly Ile Phe Leu Ala Tyr
2093	660 665 670
2094	
2095	Glu Thr Lys Ser Val Ser Thr Glu Lys Ile Asn Asp His Arg Ala Val
2096	675 680 685
2097	
2098	Gly Met Ala Ile Tyr Asn Val Ala Val Leu Cys Leu Ile Thr Ala Pro
2099	690 695 700
2100	
2101	Val Thr Met Ile Leu Ser Ser Gln Gln Asp Ala Ala Phe Ala Phe Ala
2102	705 710 715 720
2103	
2104	Ser Leu Ala Ile Val Phe Ser Ser Tyr Ile Thr Leu Val Val Leu Phe
2105	725 730 735
2106	
2107	Val Pro Lys Met Arg Arg Leu Ile Thr Arg Gly Glu Trp Gln Ser Glu
2108	740 745 750
2109	
2110	Thr Gln Asp Thr Met Lys Thr Gly Ser Ser Thr Asn Asn Asn Glu Glu
2111	755 760 765
2112	
2113	Glu Lys Ser Arg Leu Leu Glu Lys Glu Asn Arg Glu Leu Glu Lys Ile
2114	770 775 780
2115	
2116	Ile Ala Glu Lys Glu Glu Arg Val Ser Glu Leu Arg His Gln Leu Gln
2117	785 790 795 800
2118	
2119	Ser Arg Gln Gln Leu Arg Ser Arg Arg His Pro Pro Thr Pro Pro Asp

[illegible]

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SEQUENCE VERIFICATION REPORT
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Line

Error

Original Text